

SEQUENCE LISTING

<110> Sasisekharan, Ram
Shriver, Zachary
Liu, Dongfang
Venkataraman, Ganesh

<120> Rationally Designed Heparinases Derived
from Heparinase I and II

<130> M0656/7046/HCL

<150> US 60/098,153

<151> 1998-08-27

<160> 14

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2339

<212> DNA

<213> Flavobacterium heparinum

<400> 1

atgaaaagac	aattatacct	gtatgtgatt	tttgttgtag	ttgaacttat	ggttttttaca	60
acaaagggct	attcccaaac	caaggccgat	gtggtttgga	aagacgtgga	tggcgtatct	120
atgcccatat	cccctaagac	ccaccgcgt	ttgtatctac	gtgagcagca	agttcctgac	180
ctgaaaaaca	ggatgaacga	ccctaaactg	aaaaaagttt	gggccgatat	gatcaagatg	240
caggaagact	ggaagccagc	tgatattcct	gaagttaaag	actttcgttt	ttatttttaac	300
cagaaagggc	ttactgtaag	ggttgaacta	atggccctga	actatctgat	gaccaaggat	360
ccaaaggtag	gacgggaagc	catcacttca	attattgata	cccttgaaac	tgcaactttt	420
aaaccagcag	gtgatatttc	gagagggata	gtgatatttc	gagagggata	ggcctgttta	480
tggttacagg	ggccattgtg	tatgactggg	gctacgatca	gctgaaacca	gaagagaaaa	540
cacgttttgt	gaaggcattt	gtgaggctgg	ccaaaatgct	cgaatgtggt	tatcctccgg	600
taaaagacaa	gtctattgtt	gggcatgctt	ccgaatggat	gatcatgcgg	gacctgcttt	660
ctgtagggat	tgccatttac	gatgaattcc	ctgagatgta	taacctggct	gcggttcggt	720
ttttcaaaga	acacctgggt	gcccgcgaact	ggttttatcc	ctcgcataac	taccatcagg	780
gtatgtcata	cctgaacgta	agattttacca	acgacctttt	tgccctctgg	atattagacc	840
ggatgggcgc	tggtaatgtg	tttaatccag	ggcagcagtt	tatcctttat	gacgcgatct	900
ataaacgccg	ccccgatgga	cagatttttag	caggtggaga	tgtagattat	tccaggaaaa	960
aacccaaaata	ttatacgatg	cctgcattgc	ttgcaggtag	ctattataaa	gatgaatacc	1020
ttaattacga	attcctgaaa	gatcccaatg	ttgagccaca	ttgcaaattg	ttcgaaatttt	1080
tatggcgcca	taccagtggt	ggaagtcgta	agcctgatga	tttgccactt	tccaggtaact	1140
caggatcgcc	ttttggatgg	atgattgccc	gtaccggatg	gggtccggaa	agtgtgattg	1200
cagagatgaa	agtcaacgaa	tattcctttc	ttaaccatca	gcacagcatg	gcaggagcct	1260
tccagatcta	ttacaaaggc	ccgctggcca	tagatgcagg	ctcgatatac	ggttcttcag	1320
gaggtttata	acgtccgcac	aacaagaact	tttttaagcg	gactattgca	cacaatagct	1380
tgctgattta	cgatcctaaa	gaaactttca	gttcgtcggg	atatgggtga	agtgaccata	1440
ccgattttgc	tgccaacgat	gggtggtcagc	ggctgcccgg	aaaagggttg	attgcacccc	1500
gcgaccttaa	agaaatgctg	gcaggcgatt	tcaggaccgg	caaaattcct	gcccagggct	1560
ttgggtccga	taaccaaacc	cctgattata	cttatctgaa	aggagacatt	acagcagctt	1620
attcggcaaa	agtgaaggaa	gtaaaacggt	catttctatt	cctgaacctt	aaggatgcca	1680
aagttccggc	agcgatgatc	gtttttgaca	aggtagttgc	ttccaatcct	gatttttaaga	1740
agttctgggt	gttgacacagt	attgagcagc	ctgaaataaa	ggggaatcag	attaccataa	1800
aacgtacaaa	aaacggtgat	agtgggatgt	tggtgaatac	ggctttgctg	ccggatgcgg	1860

```

ccaattcaaa cattacctcc attggcggca agggcaaaga cttctgggtg tttggtacca 1920
attataccaa tgatcctaaa ccgggcacgg atgaagcatt ggaacgtgga gaatggcgtg 1980
tggaatcac tccaaaaaag gcagcagcgg aagattacta cctgaatgtg atacagattg 2040
ccgacaatac acagcaaaaa ttacacgagg tgaagcgtat tgacgggtgac aagggttggtg 2100
gtgtgcagct tgctgacagg atagttactt ttagcaaaac ttcagaaact gttgatcgtc 2160
cctttggctt ttccgttggt ggtaaaggaa cattcaaatt tgtgatgacc gatcttttag 2220
cgggtacctg gcagggtgctg aaagacggaa aaatacttta tcctgcgctt tctgcaaaag 2280
gtgatgatgg acccctttat tttgaaggaa ctgaaggaaac ctaccgtttt ttgagataa 2339

```

<210> 2

<211> 772

<212> PRT

<213> Flavobacterium heparinum

<400> 2

```

Met Lys Arg Gln Leu Tyr Leu Tyr Val Ile Phe Val Val Val Glu Leu
 1          5          10          15
Met Val Phe Thr Thr Lys Gly Tyr Ser Gln Thr Lys Ala Asp Val Val
 20          25          30
Trp Lys Asp Val Asp Gly Val Ser Met Pro Ile Pro Pro Lys Thr His
 35          40          45
Pro Arg Leu Tyr Leu Arg Glu Gln Gln Val Pro Asp Leu Lys Asn Arg
 50          55          60
Met Asn Asp Pro Lys Leu Lys Lys Val Trp Ala Asp Met Ile Lys Met
 65          70          75          80
Gln Glu Asp Trp Lys Pro Ala Asp Ile Pro Glu Val Lys Asp Phe Arg
 85          90          95
Phe Tyr Phe Asn Gln Lys Gly Leu Thr Val Arg Val Glu Leu Met Ala
100          105          110
Leu Asn Tyr Leu Met Thr Lys Asp Pro Lys Val Gly Arg Glu Ala Ile
115          120          125
Thr Ser Ile Ile Asp Thr Leu Glu Thr Ala Thr Phe Lys Pro Ala Gly
130          135          140
Asp Ile Ser Arg Gly Ile Gly Leu Phe Met Val Thr Gly Ala Ile Val
145          150          155          160
Tyr Asp Trp Cys Tyr Asp Gln Leu Lys Pro Glu Glu Lys Thr Arg Phe
165          170          175
Val Lys Ala Phe Val Arg Leu Ala Lys Met Leu Glu Cys Gly Tyr Pro
180          185          190
Pro Val Lys Asp Lys Ser Ile Val Gly His Ala Ser Glu Trp Met Ile
195          200          205
Met Arg Asp Leu Leu Ser Val Gly Ile Ala Ile Tyr Asp Glu Phe Pro
210          215          220
Glu Met Tyr Asn Leu Ala Ala Gly Arg Phe Phe Lys Glu His Leu Val
225          230          235          240
Ala Arg Asn Trp Phe Tyr Pro Ser His Asn Tyr His Gln Gly Met Ser
245          250          255
Tyr Leu Asn Val Arg Phe Thr Asn Asp Leu Phe Ala Leu Trp Ile Leu
260          265          270
Asp Arg Met Gly Ala Gly Asn Val Phe Asn Pro Gly Gln Gln Phe Ile
275          280          285
Leu Tyr Asp Ala Ile Tyr Lys Arg Arg Pro Asp Gly Gln Ile Leu Ala
290          295          300
Gly Gly Asp Val Asp Tyr Ser Arg Lys Lys Pro Lys Tyr Tyr Thr Met
305          310          315          320
Pro Ala Leu Leu Ala Gly Ser Tyr Tyr Lys Asp Glu Tyr Leu Asn Tyr
325          330          335
Glu Phe Leu Lys Asp Pro Asn Val Glu Pro His Cys Lys Leu Phe Glu

```

340							345						350					
Phe	Leu	Trp	Arg	Asp	Thr	Gln	Leu	Gly	Ser	Arg	Lys	Pro	Asp	Asp	Leu			
355							360						365					
Pro	Leu	Ser	Arg	Tyr	Ser	Gly	Ser	Pro	Phe	Gly	Trp	Met	Ile	Ala	Arg			
370							375						380					
Thr	Gly	Trp	Gly	Pro	Glu	Ser	Val	Ile	Ala	Glu	Met	Lys	Val	Asn	Glu			
385	390							395						400				
Tyr	Ser	Phe	Leu	Asn	His	Gln	His	Gln	Asp	Ala	Gly	Ala	Phe	Gln	Ile			
405							410						415					
Tyr	Tyr	Lys	Gly	Pro	Leu	Ala	Ile	Asp	Ala	Gly	Ser	Tyr	Thr	Gly	Ser			
420							425						430					
Ser	Gly	Gly	Tyr	Asn	Ser	Pro	His	Asn	Lys	Asn	Phe	Phe	Lys	Arg	Thr			
435							440						445					
Ile	Ala	His	Asn	Ser	Leu	Leu	Ile	Tyr	Asp	Pro	Lys	Glu	Thr	Phe	Ser			
450							455						460					
Ser	Ser	Gly	Tyr	Gly	Gly	Ser	Asp	His	Thr	Asp	Phe	Ala	Ala	Asn	Asp			
465	470							475						480				
Gly	Gly	Gln	Arg	Leu	Pro	Gly	Lys	Gly	Trp	Ile	Ala	Pro	Arg	Asp	Leu			
485							490						495					
Lys	Glu	Met	Leu	Ala	Gly	Asp	Phe	Arg	Thr	Gly	Lys	Ile	Leu	Ala	Gln			
500							505						510					
Gly	Phe	Gly	Pro	Asp	Asn	Gln	Thr	Pro	Asp	Tyr	Thr	Tyr	Leu	Lys	Gly			
515							520						525					
Asp	Ile	Thr	Ala	Ala	Tyr	Ser	Ala	Lys	Val	Lys	Glu	Val	Lys	Arg	Ser			
530							535						540					
Phe	Leu	Phe	Leu	Asn	Leu	Lys	Asp	Ala	Lys	Val	Pro	Ala	Ala	Met	Ile			
545	550							555						560				
Val	Phe	Asp	Lys	Val	Val	Ala	Ser	Asn	Pro	Asp	Phe	Lys	Lys	Phe	Trp			
565							570						575					
Leu	Leu	His	Ser	Ile	Glu	Gln	Pro	Glu	Ile	Lys	Gly	Asn	Gln	Ile	Thr			
580							585						590					
Ile	Lys	Arg	Thr	Lys	Asn	Gly	Asp	Ser	Gly	Met	Leu	Val	Asn	Thr	Ala			
595							600						605					
Leu	Leu	Pro	Asp	Ala	Ala	Asn	Ser	Asn	Ile	Thr	Ser	Ile	Gly	Gly	Lys			
610							615						620					
Gly	Lys	Asp	Phe	Trp	Val	Phe	Gly	Thr	Asn	Tyr	Thr	Asn	Asp	Pro	Lys			
625	630							635						640				
Pro	Gly	Thr	Asp	Glu	Ala	Leu	Glu	Arg	Gly	Glu	Trp	Arg	Val	Glu	Ile			
645							650						655					
Thr	Pro	Lys	Lys	Ala	Ala	Ala	Glu	Asp	Tyr	Tyr	Leu	Asn	Val	Ile	Gln			
660							665						670					
Ile	Ala	Asp	Asn	Thr	Gln	Gln	Lys	Leu	His	Glu	Val	Lys	Arg	Ile	Asp			
675							680						685					
Gly	Asp	Lys	Val	Val	Gly	Val	Gln	Leu	Ala	Asp	Arg	Ile	Val	Thr	Phe			
690							695						700					
Ser	Lys	Thr	Ser	Glu	Thr	Val	Asp	Arg	Pro	Phe	Gly	Phe	Ser	Val	Val			
705	710							715						720				
Gly	Lys	Gly	Thr	Phe	Lys	Phe	Val	Met	Thr	Asp	Leu	Leu	Pro	Gly	Thr			
725							730						735					
Trp	Gln	Val	Leu	Lys	Asp	Gly	Lys	Ile	Leu	Tyr	Pro	Ala	Leu	Ser	Ala			
740							745						750					
Lys	Gly	Asp	Gly	Pro	Leu	Tyr	Phe	Glu	Gly	Thr	Glu	Gly	Thr	Tyr				
755							760						765					
Arg	Phe	Leu	Arg															
770																		

```
<210> 3
<211> 1379
```

<212> DNA

<213> Flavobacterium heparinum

<220>

<221> CDS

<222> (173)...(1327)

<221> mat_peptide

<222> (236)...(1324)

<400> 3

```

ccttttggga gcaaaggcag aaccatctcc gaacaaaggc agaaccagcc tgtaaacaga      60
cagcaattca tccgctttca accaaagtga aagcatttaa tacaatacca gaatgtcgca      120
ttccctttc agcgtacttt ttgggtaaat aaccaataaa aactaaagac gg atg aaa      178
                                         Met Lys
                                         1

aaa caa att cta tat ctg att gta ctt cag caa ctg ttc ctc tgt tcg      226
Lys Gln Ile Leu Tyr Leu Ile Val Leu Gln Gln Leu Phe Leu Cys Ser
                    5                      10                      15

gct tac gcc cag caa aaa aaa tcc ggt aac atc cct tac cgg gta aat      274
Ala Tyr Ala Gln Gln Lys Lys Ser Gly Asn Ile Pro Tyr Arg Val Asn
                    20                      25                      30

gtg cag gcc gac agt gct aag cag aag gcg att att gac aac aaa tgg      322
Val Gln Ala Asp Ser Ala Lys Gln Lys Ala Ile Ile Asp Asn Lys Trp
                    35                      40                      45                      50

gtg gca gta ggc atc aat aaa cct tat gca tta caa tat gac gat aaa      370
Val Ala Val Gly Ile Asn Lys Pro Tyr Ala Leu Gln Tyr Asp Asp Lys
                    55                      60                      65

ctg cgc ttt aat gga aaa cca tcc tat cgc ttt gag ctt aaa gcc gaa      418
Leu Arg Phe Asn Gly Lys Pro Ser Tyr Arg Phe Glu Leu Lys Ala Glu
                    70                      75                      80

gac aat tcg ctt gaa ggt tat gct gca gga gaa aca aag ggc cgt aca      466
Asp Asn Ser Leu Glu Gly Tyr Ala Ala Gly Glu Thr Lys Gly Arg Thr
                    85                      90                      95

gaa ttg tcg tac agc tat gca acc acc aat gat ttt aag aaa ttt ccc      514
Glu Leu Ser Tyr Ser Tyr Ala Thr Thr Asn Asp Phe Lys Lys Phe Pro
                    100                      105                      110

cca agc gta tac caa aat gcg caa aag cta aaa acc gtt tat cat tac      562
Pro Ser Val Tyr Gln Asn Ala Gln Lys Leu Lys Thr Val Tyr His Tyr
                    115                      120                      125                      130

ggc aaa ggg att tgt gaa cag ggg agc tcc cgc agc tat acc ttt tca      610
Gly Lys Gly Ile Cys Glu Gln Gly Ser Ser Arg Ser Tyr Thr Phe Ser
                    135                      140                      145

gtg tac ata ccc tcc tcc ttc ccc gac aat gcg act act att ttt gcc      658
Val Tyr Ile Pro Ser Ser Phe Pro Asp Asn Ala Thr Thr Ile Phe Ala
                    150                      155                      160

caa tgg cat ggt gca ccc agc aga acg ctt gta gct aca cca gag gga      706

```

Gln Trp His Gly Ala Pro Ser Arg Thr Leu Val Ala Thr Pro Glu Gly	
165 170 175	
gaa att aaa aca ctg agc ata gaa gag ttt ttg gcc tta tac gac cgc	754
Glu Ile Lys Thr Leu Ser Ile Glu Glu Phe Leu Ala Leu Tyr Asp Arg	
180 185 190	
atg atc ttc aaa aaa aat atc gcc cat gat aaa gtt gaa aaa aaa gat	802
Met Ile Phe Lys Lys Asn Ile Ala His Asp Lys Val Glu Lys Lys Asp	
195 200 205 210	
aag gac gga aaa att act tat gta gcc gga aag cca aat ggc tgg aag	850
Lys Asp Gly Lys Ile Thr Tyr Val Ala Gly Lys Pro Asn Gly Trp Lys	
215 220 225	
gta gaa caa ggt ggt tat ccc acg ctg gcc ttt ggt ttt tct aaa ggg	898
Val Glu Gln Gly Gly Tyr Pro Thr Leu Ala Phe Gly Phe Ser Lys Gly	
230 235 240	
tat ttt tac atc aag gca aac tcc gac cgg cag tgg ctt acc gac aaa	946
Tyr Phe Tyr Ile Lys Ala Asn Ser Asp Arg Gln Trp Leu Thr Asp Lys	
245 250 255	
gcc gac cgt aac aat gcc aat ccc gag aat agt gaa gta atg aag ccc	994
Ala Asp Arg Asn Asn Ala Asn Pro Glu Asn Ser Glu Val Met Lys Pro	
260 265 270	
tat tcc tcg gaa tac aaa act tca acc att gcc tat aaa atg ccc ttt	1042
Tyr Ser Ser Glu Tyr Lys Thr Ser Thr Ile Ala Tyr Lys Met Pro Phe	
275 280 285 290	
gcc cag ttc cct aaa gat tgc tgg att act ttt gat gtc gcc ata gac	1090
Ala Gln Phe Pro Lys Asp Cys Trp Ile Thr Phe Asp Val Ala Ile Asp	
295 300 305	
tgg acg aaa tat gga aaa gag gcc aat aca att ttg aaa ccc ggt aag	1138
Trp Thr Lys Tyr Gly Lys Glu Ala Asn Thr Ile Leu Lys Pro Gly Lys	
310 315 320	
ctg gat gtg atg atg act tat acc aag aat aag aaa cca caa aaa gcg	1186
Leu Asp Val Met Met Thr Tyr Thr Lys Asn Lys Lys Pro Gln Lys Ala	
325 330 335	
cat atc gta aac cag cag gaa atc ctg atc gga cgt aac gat gac gat	1234
His Ile Val Asn Gln Gln Glu Ile Leu Ile Gly Arg Asn Asp Asp Asp	
340 345 350	
ggc tat tac ttc aaa ttt gga att tac agg gtc ggt aac agc acg gtc	1282
Gly Tyr Tyr Phe Lys Phe Gly Ile Tyr Arg Val Gly Asn Ser Thr Val	
355 360 365 370	
ccg gtt act tat aac ctg agc ggg tac agc gaa act gcc aga tag	1327
Pro Val Thr Tyr Asn Leu Ser Gly Tyr Ser Glu Thr Ala Arg *	
375 380	
caaaagccct aagcgcaccc gatagggtt ttcttatatt tacaataaaa tt	1379

<400> 4															
Met 1	Lys	Lys	Gln	Ile 5	Leu	Tyr	Leu	Ile	Val 10	Leu	Gln	Gln	Leu	Phe 15	Leu
Cys	Ser	Ala	Tyr	Ala	Gln	Gln	Lys	Lys	Ser	Gly	Asn	Ile	Pro	Tyr	Arg
			20			25						30			
Val	Asn	Val	Gln	Ala	Asp	Ser	Ala	Lys	Gln	Lys	Ala	Ile	Ile	Asp	Asn
			35			40						45			
Lys	Trp	Val	Ala	Val	Gly	Ile	Asn	Lys	Pro	Tyr	Ala	Leu	Gln	Tyr	Asp
			50			55						60			
Asp	Lys	Leu	Arg	Phe	Asn	Gly	Lys	Pro	Ser	Tyr	Arg	Phe	Glu	Leu	Lys
65				70			75						80		
Ala	Glu	Asp	Asn	Ser	Leu	Glu	Gly	Tyr	Ala	Gly	Glu	Thr	Lys	Gly	
			85			90						95			
Arg	Thr	Glu	Leu	Ser	Tyr	Ser	Tyr	Ala	Thr	Thr	Asn	Asp	Phe	Lys	Lys
			100			105						110			
Phe	Pro	Pro	Ser	Val	Tyr	Gln	Asn	Ala	Gln	Lys	Leu	Lys	Thr	Val	Tyr
			115			120						125			
His	Tyr	Gly	Lys	Gly	Ile	Cys	Glu	Gln	Gly	Ser	Ser	Arg	Ser	Tyr	Thr
			130			135						140			
Phe	Ser	Val	Tyr	Ile	Pro	Ser	Ser	Phe	Pro	Asp	Asn	Ala	Thr	Thr	Ile
145				150			155						160		
Phe	Ala	Gln	Trp	His	Gly	Ala	Pro	Ser	Arg	Thr	Leu	Val	Ala	Thr	Pro
			165			170						175			
Glu	Gly	Glu	Ile	Lys	Thr	Leu	Ser	Ile	Glu	Glu	Phe	Leu	Ala	Leu	Tyr
			180			185						190			
Asp	Arg	Met	Ile	Phe	Lys	Lys	Asn	Ile	Ala	His	Asp	Lys	Val	Glu	Lys
			195			200						205			
Lys	Asp	Lys	Asp	Gly	Lys	Ile	Thr	Tyr	Val	Ala	Gly	Lys	Pro	Asn	Gly
			210			215						220			
Trp	Lys	Val	Glu	Gln	Gly	Gly	Tyr	Pro	Thr	Leu	Ala	Phe	Gly	Phe	Ser
225				230			235						240		
Lys	Gly	Tyr	Phe	Tyr	Ile	Lys	Ala	Asn	Ser	Asp	Arg	Gln	Trp	Leu	Thr
			245			250						255			
Asp	Lys	Ala	Asp	Arg	Asn	Asn	Ala	Asn	Pro	Glu	Asn	Ser	Glu	Val	Met
			260			265						270			
Lys	Pro	Tyr	Ser	Ser	Glu	Tyr	Lys	Thr	Ser	Thr	Ile	Ala	Tyr	Lys	Met
			275			280						285			
Pro	Phe	Ala	Gln	Phe	Pro	Lys	Asp	Cys	Trp	Ile	Thr	Phe	Asp	Val	Ala
			290			295						300			
Ile	Asp	Trp	Thr	Lys	Tyr	Gly	Lys	Glu	Ala	Asn	Thr	Ile	Leu	Lys	Pro
305				310			315						320		
Gly	Lys	Leu	Asp	Val	Met	Met	Thr	Tyr	Thr	Lys	Asn	Lys	Lys	Pro	Gln
			325			330						335			
Lys	Ala	His	Ile	Val	Asn	Gln	Gln	Glu	Ile	Leu	Ile	Gly	Arg	Asn	Asp
			340			345						350			
Asp	Asp	Gly	Tyr	Tyr	Phe	Lys	Phe	Gly	Ile	Tyr	Arg	Val	Gly	Asn	Ser
			355			360						365			
Thr	Val	Pro	Val	Thr	Tyr	Asn	Leu	Ser	Gly	Tyr	Ser	Glu	Thr	Ala	Arg
			370			375						380			

```
<210> 5
<211> 10
<212> PRT
<213> Flavobacterium heparinum
```

<400> 5

Lys Asp Pro Asn Val Glu Pro His Cys Lys
 1 5 10

<210> 6

<211> 34

<212> PRT

<213> Flavobacterium heparinum

<400> 6

Lys Tyr Tyr Thr Met Pro Ala Leu Leu Ala Gly Ser Tyr Tyr Lys Asp
 1 5 10 15
 Glu Tyr Leu Asn Tyr Glu Phe Leu Lys Asp Pro Asn Val Glu Pro His
 20 25 30
 Cys Lys

<210> 7

<211> 14

<212> PRT

<213> Flavobacterium heparinum

<400> 7

Arg Thr Ile Ala His Asn Ser Leu Leu Ile Tyr Asp Pro Lys
 1 5 10

<210> 8

<211> 15

<212> PRT

<213> Flavobacterium heparinum

<400> 8

Lys Arg Thr Ile Ala His Asn Ser Leu Leu Ile Tyr Asp Pro Lys
 1 5 10 15

<210> 9

<211> 7

<212> PRT

<213> Flavobacterium heparinum

<400> 9

Lys Glu His Leu Val Ala Arg
 1 5

<210> 10

<211> 14

<212> PRT

<213> Flavobacterium heparinum

<400> 10

Lys Phe Trp Leu Leu His Ser Ile Glu Gln Pro Glu Ile Lys
 1 5 10

<210> 11

<211> 7

<212> PRT

<213> Flavobacterium heparinum

<400> 11

Lys Ala Ile Ile Asp Asn Lys
 1 5

<210> 12

<211> 13

<212> PRT

<213> Flavobacterium heparinum

<400> 12

Lys Asn Ile Ala His Asp Lys Val Glu Lys Lys Asp Lys
 1 5 10

<210> 13

<211> 10

<212> PRT

<213> Flavobacterium heparinum

<400> 13

Arg Val Asn Val Gln Ala Asp Ser Ala Lys
 1 5 10

<210> 14

<211> 26

<212> PRT

<213> Flavobacterium heparinum

<400> 14

Lys Phe Gly Ile Tyr Arg Val Gly Asn Ser Thr Val Pro Val Thr Tyr
 1 5 10 15
 Asn Leu Ser Gly Tyr Ser Glu Thr Ala Arg
 20 25